

SUBSTITUTE SHEET (RULE 26)

<u>2/24</u>

		10	20	30	40	50	
MOUSE-X1.DNA	1	ATGAGGCTTC	CTGGTTGGTT	GTGGCTGAGT	TCTGCCGTCC	TCGCTGCCTG	50
HUMAN-X1.DNA	1	ATGAAGCTGG	CTAACTGGTA	CTGGCTGAGC	TCAGCTGTTC	TTGCCACTTA	50
		60	70	80	90	100	
MOUSE-X1.DNA	51	CCGAGCG	GTGGAGGAGC	ACAACCTGAC	TGAGGGGCTG	GAGGATGCCA	100
HUMAN-X1.DNA	51	CGGTTTTTTG	GTTGTGGCAA	ACAATGAAAC	AGAGGAAATT	aaagatgaaa	100
		110	120	130	140	150	
MOUSE-X1.DNA	101	GCGCCCAGGC	TGCCTGCCCC	GCGAGGCTGG	AGGGCAGCGG	GAGGTGCGAG	150
HUMAN-X1.DNA	101	GAGCAAAGGA	TGTCTGCCCA	GTGAGACTAG	AAAGCAGAGG	GAAATGCGAA	150
		160	170	180	190	200	
MOUSE-X1.DNA	151	GGGAGCC	AGTGCCCCTT	CCAGCTCACC	CTGCCCACGC	TGACCATCCA	200
HUMAN-X1.DNA	151	GAGGCAGGGG	AGTGCCCCTA	CCAGGTAAGC	CTGCCCCCT	TGACTATTCA	200
		210	220	230	240	250	
MOUSE-X1.DNA	201	GCTCCCGCGG	CAGCTTGGCA	GCATGGAGGA	GGTGCTCAAA	GAAGTGCGGA	250
HUMAN-X1.DNA	201	GCTCCCGAAG	CAATTCAGCA	GGATCGAGGA	GGTGTTCAAA	GAAGTCCAAA	250
		260	270	280	290	300	
MOUSE-X1.DNA	251	CCCTCAAGGA	AGCAGTGGAC	AGTCTGAAGA	AATCCTGCCA	GGACTGTAAG	300
HUMAN-X1.DNA	251	ACCTCAAGGA	AATCGTAAAT	AGTCTAAAGA	AATCTTGCCA	AGACTGCAAG	300
		310	320	330	340	350	
MOUSE-X1.DNA	301	TTGCAGGCTG	ACGACCATCG	AGATCCCGGC	GGGAATGGAG	GG	350
HUMAN-X1.DNA	301	CTGCAGGCTG	ATGACAACGG	AGACCCAGGC	AGAAACGGAC	TGTTGTTACC	350
		360	370	380	390	400	
MOUSE-X1.DNA	351	-AATGGA	GCAGAGA	CAGCCGAGGA	CAGTAGAGTC	CAGGAACTGG	400
HUMAN-X1.DNA	351	CAGTACAGGA	GCCCCGGGAG	AGGTTGGTGA	TAACAGAGTT	AGAGAATTAG	400
		410	420	430	440	450	
MOUSE-X1.DNA	401	AGAGTCAGGT	GAACAAGCTG	TCCTCAGAGC	TGAAGAATGC	AAAGGACCAG	450
HUMAN-X1.DNA	401	AGAGTGAGGT	TAACAAGCTG	TCCTCTGAGC	TAAAGAATGC	CAAAGAGGAG	450
		460	470	480	490	500	
MOUSE-X1.DNA				CCTGGAGACG			500
HUMAN-X1.DNA	451	ATCAATGTAC	TTCATGGTCG	CCTGGAGAAG	CTGAATCTTG	TAAATATGAA	500
		510	520	530	540	550	
MOUSE-X1.DNA				ACAACAAAGT			550
HUMAN-X1.DNA	501	CAACATAGAA	AATTATGTTG	ACAGCAAAGT	GGCAAATCTA	ACATTTGTTG	550
		560	570	580	590	600	
MOUSE-X1.DNA	551	TCAACAGTTT	GGATGGCAAG	TGTTCCAAGT	GTCCCAGCCA	AGAACACATG	600
HUMAN-X1.DNA	551	TCAATAGTTT	GGATGGCAAA	TGTTCAAAGT	GTCCCAGCCA	AGAACAAATA	600
		610	620	630	640	650	
MOUSE-X1.DNA	601	CAGTCACAGC	CGG				650
HUMAN-X1.DNA	601	CAGTCACGTC	CAG				650

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		10	20	30	40	50	
MOUSE-X2.DNA	1		AATATACAAA	GATTGTTCCG	ACCACTACGT	GCTAGGAAGG	50
HUMAN+X2.DNA	1	TTCAACATCT	AATATATAAA	GATTGCTCTG	ACTACTACGC	AATAGGCAAA	50
HOLDIN ALIBINI		60	70	80	90	100	
MOUSE-X2.DNA	51	AGAAGCAGTG	GGGCCTACAG	AGTTACCCCT	GATCACAGAA	ACAGCAGCTT	100
HUMAN-X2.DNA	51	AGAAGCAGTG	AGACCTACAG	AGTTACACCT	GATCCCAAAA	ATAGTAGCTT	100
		110	120	130	140	150	
MOUSE-X2.DNA	101	TGAGGTCTAC	TGTGACATGG	AGACCATGGG	TGGAGGCTGG	ACGGTGCTGC	150
HUMAN-X2.DNA	101	TGAAGTTTAC	TGTGACATGG				150
		160	170	180	190	200	
MOUSE-X2.DNA	151	AGGCTCGCCT	TGATGGCAGC	ACCAACTTCA	CCAGAGAGTG	GAAAGACTAC	200
HUMAN-X2.DNA	151	AGGCACGTCT	CGATGGGAGC				200
		210	220	230	240	250	
MOUSE-X2.DNA	201	AAAGCCGGCT	TTGGAAACCT	TGAACGAGAA	TTTTGGTTGG	GCAACGATAA	250
HUMAN-X2.DNA	201	AAAGCAGGCT	TTGGAAACCT		TTTTGGCTGG	GGAACGATAA	250
		260	270	280	290	300	300
MOUSE-X2.DNA	251	AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTTTGAGA	ATAGATCTTG	300
HUMAN-X2.DNA	251		CTGACCAAGA		GATTUTGAGA 340	350	300
		310	320	330	•		350
MOUSE-X2.DNA	301	AAGACTTTAA	TGGTCTCACA	CTTTATGCCT	TGTATGATCA	CTTTTTATGTG	350
HUMAN-X2.DNA	301		TGGTGTCGAA	CTATATGCCT	390	400	330
		360	370 TTCTCAAATA				400
MOUSE-X2.DNA	351	GCTAATGAAT	TTCTCAAATA	TCCGATTACAC	GTTGGTAACT	ATAATGGCAC	400
HUMAN-X2.DNA	351			430	440	450	
	401	410	GCCTTGCGTT		• • •		450
MOUSE-X2.DNA	401	TADDDDDAJDJ .	GCCTTGCGTT	TCAACAAACA	TTACAACCAC	GATCTGAAGT	450
HUMAN-X2.DNA	401	AGCIGGAGAI 460		480	490	500	
MOUSE-X2.DNA	453	יטוב ממממתיתיים	CCCAGACAGA	GACAACGATC	GGTACCCCTC	TGGGAACTGT	500
HUMAN-X2.DNA	451	TITICACAAC	TCCAGATAAA	GACAATGATC	GATATCCTTC	TGGGAACTGT	500
HOMAN-X2.DNA	401	510			540	550	
MOUSE-X2.DNA	501	GGGCTCTATI	ACAGCTCAGG	CTGGTGGTTT	GATTCATGTC	TCTCTGCCAA	550
HUMAN-X2.DNA		GGGCTGTACT		CIGGIGGIII	GATGCATGTC	TTTCTGCAAA	550
		560	570			600	
MOUSE-X2.DNA	55	1 CTTAAATGG	AAATATTACO	ACCAGAAATA	CAAAGGTGTC	CGTAATGGGA	600
HUMAN-X2.DNA	55	1 CTTAAATGG	AAATATTATC	ACCAAAAATA	. CAGAGGTGTC	CGTAATGGGA	600
		610	620				
MOUSE-X2.DNA	60	1 TTTTCTGGG	G CACCTGGCC1	GGTATAAACC	AGGCACAGCC	AGGTGGCTAC	650
HUMAN-X2.DNA	60	1 TTTTCTGGG	G TACCTGGCC1	GGTGTAAGTG	AGGCACACCC	TGGTGGCTAC	650
		66	0 670				222
MOUSE-X2.DNA	65	1 AAGTCCTCC	T TCAAACAGG	CAAGATGAT	ATTAGGCCCA	AGAATTTCAA	700
HUMAN-X2.DNA	65	1 AAGTCCTCC	T TCAAAGAGGG			AGCACTTTAA	700
		71	0 720	0 730	740	750	750
MOUSE-X2.DNA	70	1 GCCATAA					750
HUMAN-X2.DNA	70	1 GCCATAA		• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • •	130

10	20	30	40	50	60
ATCACTCTGT	TCATTCCTCC	AGGTATTCGT	TATCTAATAG	GGCAATTAAT	TCCTTCAGCA
70	80	90	100	110	120
CTTTAGAATA	TGCCTTGTTT	CATATTTTTC	ATAGCTAAAA	AATGCCTTGT	TTCATATTTT
130	140	150	160	170	180
TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	CTACACAGCA	TTTGAAATAA
190	200	210	220	230	240
AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	ATGCTGTTAT	CCAATGAACA
250	260	270	280	290	300
CTTGCAAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	TTACAATTCT	TTTAATTTCT
310	320	330	340	350	360
ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	TAATAAAAA	TGTTGGCTGG
370	380	390	400	410	420
GTGTGGTAGC	TCACGCCTGT	AATNCCAGCA	CTTTGGAATG	TCAAGGCAGG	
430	440	450	460	470	480
GAGGTCAGGA	GTTTGAGACC			ACGCTGTNTN	
490	500	510	520	530	540
ACAAAAATTA	GCCGGGCATG	GTGGNACATG		TAGNTACTTG	
550	560	570	580	590	600
GCAGGAGAAT	CGCTTGAACC			GAGCCAAGAA	
610	620	630	640	650	660
CACTCCAGCA	TGGGTGACAG			AAAAAATAAT	
670	680	690	700	710	720
CAGTAGGNTG	GATTCTACAC				GCACATCTGA
730	740	750	760		780
AGGTATATCA			TTTGGGTAAT		
790			820		840
AATCTATATC		•	ACCCTACAGO		
850					900
GGAACTAATA	_				TAAAATI.CTT 960
910					
GTCATTTAAA		ATGTGGTAGO		CCCAAAAAGC	
970	- '				
CAATGTAACT					
1030					1080
ATGTTTGAT	TTGAAAACT	CTTTAACATO	3 AA	• • • • • • • • • •	• • • • • • • • •

3'UTR of hfgl2. The A at position 1 corresponds to position 1354 on the cDNA.

<u>5/24</u>

			10	20	30	40	50	
	MOUSEPRO.AMI	1	REPGALALS	SAVLAACR-A	Veehal regl	ERASAQAA	ARMEGS RE	50
	HUMANPRO.AMI	1	KLANAYNLS	SAVLATYGEL	VVANRENSEI	KUERAKDVE	VELLESREKEE	50
			60	70	80	90	100	
	MOUSEPRO.AMI	51	-GSQCIFFLT	LFT LTIOLER	LGSMEEVLA	EVRTLKEAVD	SLKKSCODCK	100
	HUMANPRO.AMI	51	EAGE Y VS	TES LT IOTEK	FSRIFEVER	EVON LKE I V N	SLKKSCODCK	100
			110	120	130	140	150	
	MOUSEPRO.AMI	101	LOADDHRDPG	GNGGN	GAETAELSRV	CELESOVNKI	SSELKNAKDQ	150
	HUMANPRO.AMI	101	LOADDNEDPG	RNGLLLPSTG	APGEVGENEV	RELESEVNKL	SSELKNAKEE	150
			160	170	180	190	200	
	MOUSEPRO.AMI	151	IOGLOGRLET	LELVNMNNIE	NYVD <u>N</u> KVANL	TVVVNSLDGK	CSKCPSOEHM	200
	HUMANPRO.AMI	151	INV HERLEK	LNLVNMNNIE	NAADSKAVUT	TEVVNSLDGK	CSKCPSOEDI	200
			210	220	230	240	250	
	MOUSEPRO.AMI	201	⊋S⊚PVOHLIY	KDCSDHYVLS	RRSSGAYRVT	PDHRNSSFEV	YCDMETMGGG	250
	HUMANPRO.AMI	201	DSRPVQHLIY	KDCSDYYAIS	KRSSETYRVT	PDPKNSSFEV	YCDMETMGGG	250
·IJ			260	270	280	290	300	
i mo	MOUSEPRO.AMI	251	NTVLQARLDG	STNFTREAKC	YKAGFGNLEP	EFWLGNDKIH	LLTKSKEMIL	300
	HUMANPRO.AMI	251	MTVLQARLDG	STNFTPTACL	YKAGFGNLRF	EFWLGNDKIH	LLTKSKEMIL	300
FF			310	320	330	340	350	
	MOUSEPRO.AMI	301	RIDLEDENGL	TLYALYDOFY	VANEFLKYRL	HIGNYNGTAG	DALRESPHYN	350
111	HUMANPRO.AMI	301	RIDLEDENGV	ELYALYDOFY	VANEFLKYRL	HVGNYNGTAG	DALRENKHYN	350
51			360	370	380	390	400	
- Territoria	MOUSEPRO.AMI	351	HDLRFFTTPD	RONDRYPSGN	CGLYYSSGWW	FUSCLSANLN	GKYYHQKY ₹3	400
1-1	HUMANPRO.AMI	351	HDLKFFTTPD	KONDRYPSGN	CGLYYSSGWW	FLACLSANLN	GKYYHQKYRS	400
			410	420	430	440	450	
577 E	MOUSEPRO.AMI	401	VRNGIFWGTW		YKSSFKCAKM	MIRPKNEKP*	• • • • • • • • • • •	450
	HUMANPRO.AMI	401	VRNGIFWGTW	PGVSEAHPGG	YKSSFKBAKM	MIRPK#FKP*		450

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	50	40	30	20	10		
50	ARLEGSGRCE	EDASAQAACP	VEEHNLTEGL	SAVLAACR-A	MRLPGWLWLS	1	MOUSEPRO.AMI
50	VRLESRGKCE	KDERAKDVCP	VVANNETEEI	SAVLATYGFL	MKLANWYWLS	1	HUMANPRO.AMI
30	100	90	80		60		
100		EVRTLKEAVD	QLGSMEEVLK	LPTLTIQLPR	-GSQCPFQLT	51	MOUSEPRO.AMI
100	SLKKSCODCK	EVQNLKEIVN	QFSRIEEVFK	LPPLTIQLPK	EAGECPYQVS	51	HUMANPRO.AMI
100	150	140	130		110		
150	SSELKNAKDO	QELESOVNKL	GAETAEDSRV	GNGGN	LQADDHRDPG	101	MOUSEPRO.AMI
150	SSELKNAKEE	RELESEVNKL	APGEVGDNRV	RNGLLLPSTG	LQADDNGDPG	101	HUMANPRO.AMI
130	200	190	180	170	160		
200		TVVVNSLDGK	NYVDNKVANL	LHLVNMNNIE	IQGLQGRLET	151	MOUSEPRO.AMI
200	CSKCPSOEOT	TFVVNSLDGK	NYVDSKVANL	LNLVNMNNIE	INVLHGRLEK	151	HUMANPRO.AMI
200	250	240	230	220	210		
250		PDHRNSSFEV	RRSSGAYRVT	KDCSDHYVLG	QSQPVQHLIY	201	MOUSEPRO.AMI
250	YCDMETMGGG	PDPKNSSFEV	KRSSETYRVT	KDCSDYYAIG	QSRPVQHLIY	201	HUMANPRO.AMI
230	300	290	280	270	260		
300		EFWLGNDKIH	YKAGFGNLER	STNFTREWKD	WTVLQARLDG	251	MOUSEPRO.AMI
300				STNFTRTWQD			HUMANPRO.AMI
300	350	340	330	320	310		
350		HIGNYNGTAG	VANEFLKYRL	TLYALYDQFY	RIDLEDFNGL	301	MOUSEPRO.AMI
350	DALRENKHYN	HVGNYNGTAG	VANEFLKYRL	ELYALYDQFY	RIDLEDFNGV	301	HUMANPRO.AMI
330	400	390	380	370	360		
400		FDSCLSANLN	CGLYYSSGWW	RDNDRYPSGN	HDLRFFTTPD	351	MOUSEPRO.AMI
400	GKYYHOKYRG	FDACLSANLN	CGLYYSSGWW	KDNDRYPSGN	HDLKFFTTPD	351	HUMANPRO.AMI
400	450	440	430	420	410		
450	• • • • • • • • •		YKSSFKQAKM	PGINQAQPGG	VRNGIFWGTW	401	MOUSEPRO.AMI
450	• • • • • • • • •	MIRPKHFKP*	YKSSFKEAKM	PGVSEAHPGG	VRNGIFWGTW	401	HUMANPRO.AMI
320							

		10	20	30	40	50	60	70
	HKLAHWYN	TLSSAVL)	ATYGFLVV	nnet ee i kdei	RAKDVCPVRL	ESRGKCZEAG	ECPYOVSLP	LTIOLPK
HELIX	KHhhhhhh	ותממממה	ռիռեռերե	нниннии	1HH			hh
SHEET	335333	333333	******		SSSSSS		3335555	
TURN		:	TTTT	IIII	•	TITITI		TT TTT
COIL					С	ccc		•••
							•	
		80	90	100	110	120	130	140
	QFSRIEEV	FREVQN	LKEIVNSL	KKSCODCKLQA	DDNGDPGRNG	LLLPSTGAPG	EVGDNRVRE	ESEVERT.
HELIX	НИКНИНН	ннинин	нинн					HHHH
SHEET	8823333	333833	3333333	352		2 S 2	******	
TORN				TITTITIT TI			*************	
COIL								ccc
		150	160	170	180	190	200	210
	SSELKNA	KEEIHVL	HGRLEKLN	LVNHNNIENYV				2 TU
HELIX	жини	ннныын	նինդեր	hhhh	հերերեր			_
SHEET		SSSa		222222222				hhhhhhhh SSSSSSs
TURN			TTTT		TITT	IIIIIIII		
COIL	cc					********	.1111	I
		220	230	240	250	260	270	280
	KDCSDYY	AIGKRSS	ETYRVTPE	PKHSSFEVYCD				200
HELIX	h					հերհեր	hhhH	ннн Худио 10л
SHEET		33	35555	s53555		SSSSs	3SS33	ппл
	1111111			TITTI	TITTIT	TITIT	TTTTT T	cccc
TURN							TTTTT T	cccc
TURN	1111111					TITIT	TTTTT	
TURN	1111111	TTTTT	300	310	TITTT 320	330	340	350
TURN	EFWLGHD	TTTTT 290 KIHLLTE	300 SKEMILRI	TTTTTT 310 DLEDFNGVELY	TIITIT 320 (ALYDOFYVA)	TITTT: 330 EFLKYRLHV	340	350
TURN COIL HELIX	EFWLGHD	TTTTT 290 KIHLLTE	300 SKEMILRI	TTTTTT 310 DLEDFXGVELY NAHKDANANA	TITTTT 320 (ALYDOFYVAL) Shibbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbb	TITIT 330 EFLKYRLHV Jhhhh	TTTTT 340 GNYNGTAGDA	350
TURN COIL HELIX	TITITITI EFWLGHE	TTTTT 290 KIHLLT: hhhhhh	300 KSKEMILRI	310 (DLEDFNGVEL) (DHHADADADA (SS) SSS	TIITIT 320 (ALYDOFYVA)	330 IEFLKYRLHV JANAH SSSSSSSSS	TTTTT 340 SHYNGTAGDA	350 Lrенкнұн
TURN COIL HELIX SHEET	EFWLGNE HHHh	TTTTT 290 KIHLLT: hhhhhh	300 KSKEMILRI SSSSS	TTTTTT 310 DLEDFXGVELY NAHKDANANA	TITTTT 320 (ALYDOFYVAL) Shibbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbb	330 IEFLKYRLHV JANAH SSSSSSSSS	340 SHYNGTAGDA	350 LRENKHYN TITIT
TURN COIL HELIX SHEET TURN	EFWLGNE HHHh	TTTTT 290 KIHLLT: hhhhhh	300 KSKEMILRI SSSSS	310 (DLEDFNGVEL) (DHHADADADA (SS) SSS	TITTTT 320 (ALYDOFYVAL) Shibbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbb	330 IEFLKYRLHV JANAH SSSSSSSSS	340 SHYNGTAGDA	350 Lrenkhyn
TURN COIL HELIX SHEET TURN	EFWLGNE HHHh	TTTTT 290 KIHLLT: hhhhhh	300 KSKEMILRI SSSSS	310 (DLEDFNGVEL) (DHHADADADA (SS) SSS	TITTTT 320 (ALYDOFYVAL) Shibbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbbb	TITTT 330 IEFLKYRLHV IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	340 SNYNGTAGDA	350 LRENKHYN TITTT CCC
TURN COIL HELIX SHEET TURN	EFWLGND HHHh SSSS TTTT	TTTTT 290 PKIHLLTE hhhhhhh SSSSS T TT	300 KSKEMILRI Inhikhhhhh SSSSI ITT	310 DLEDFRGVELY THERBORN SSS TITT 380	J20 (ALYDOFYVAL hhhhhhhhhhhh issssssss	TITTIT	340 SHYNGTAGDA ITTITITIT C	350 LRENKHYN TITIT CCC
TURN COIL HELIX SHEET TURN COIL	EFWLGND HHHh SSSS TTTT	TTTTT 290 KIHLLTE hhhhhhi SSSSS T TT 360 TTPDKDNE	300 KSKEMILRI Inhikhhhhh SSSSI ITT	310 (DLEDFNGVEL) hhhhhhhhhhhhh 5S3 SSS TTTT 380 GLYYSSGWWFD	J20 (ALYDOFYVAL hhhhhhhhhh BSSSSSSSSSSSSSSSSSSSSSSSSSS	TITTIT	340 SNYNGTAGDA ITTITITIT C 410 NGIFWGTWFG	350 LRENKHYN TITIT CCC 420 VSEAHPGG
TURN COIL HELIX SHEET TURN COIL	EFWLGND HHHh SSS TTTT	TTTTT 290 KIHLLTE hhhhhhl SSSS T TT 360 TTPDKDNE	300 KSKEMILRI Inhikhhhhh SSSSI ITT	310 (DLEDFNGVEL) hhhhhhhhhhh 5Ss SSS TITT 380 GLYYSSGWWFD	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	JJO SEFLKYRLHV SSSSSSSSS TT 400 YYHQKYRGVR	340 SHYNGTAGDA ITTITITI C 410 HGIFHGIHPG	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEETS	EFWLGND HHHh SSSS TTTT HOLKFFT	TTTTT 290 PKIHLLTE hhhhhhl SSSSS TTTT 360 TTPDKDNE	300 KSKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEETS	EFWLGND HHHh SSSS TTTT HOLKFFT hhhhhh	TTTTT 290 PKIHLLTE hhhhhhl SSSSS TTTT 360 TTPDKDNE	300 KSKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 SHYNGTAGDA TTTTTTTT C 410 HGIFHGTHPG	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGND HHHh SSSS TTTT HOLKFFT hhhhhh	TTTTT 290 PKIHLLTE hhhhhhl SSSSS TTTT 360 TTPDKDNE	300 KSKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGND HHHh SSSS TTTT HOLKFFT hhhhhh	TTTTT 290 PKIHLLTE hhhhhhl SSSSS TTTT 360 TTPDKDNE	300 KSKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGND HHHh HDLKFFT hhhhhh SSSSS	TTTTT 290 PKIHLLTE hhhhhhh SSSSS T TT 360 TPDKDNI hh SS	300 KSKEMILRI SSSSSITT 370 DRYPSGNC	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGND HHHh HDLKFFT hhhhhi sasss	TTTTT 290 PKIHLLTE hhhhhhh SSSSS T TT 360 TPDKDNI hh SS	300 KSKEMILRI SSSSSITT 370 DRYPSGNC	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGHD HHHH HDLKFFT hhhhhh sasss TITT YKSSFK	TTTTT 290 PKIHLLTE hhhhhhh SSSSS T TT 360 TPDKDNI hh SS TTTTTTT 430 EARDMIR	300 KSKEMILRI SSSSSITT 370 DRYPSGNC	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGND HHHH HDLKFFT hhhhhh sasss TITT YKSSEK	290 PKIHLLTE Phhhhhhi SSSSS T TT 360 TPDKDNI TTTTTT 430 EARDMIR HHHHHH	300 KSKEMILRI SSSSSITT 370 DRYPSGNC	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGND HHHH HDLKFFT hhhhhi sasss TIT YKSSFK K hhi TITITT	290 PKIHLLTE Phhhhhhi SSSSS T TT 360 TPDKDNI TTTTTT 430 EARDMIR HHHHHH	300 KSKEMILRI Shhhkhhhhh SSSS: ITT 370 DRYPSGNC	310 (DLEDFNGVEL) hhHbhhhbhhh SS3 SSS TTTT 380 GLYYSSGWWFD: hhhi ass sss	J20 (ALYDOFYVAL hhhhhhhhhhh sssssssss 390 ACLSANLRGE	330 IEFLKYRLHV IIIII IIIII IIIIII IIIIII IIIIII IIIIII	340 GNYNGTAGDA TTTTTTTT C 410 NGIFWGTWPG bh	350 LRENKHYN TITIT CCC 420 VSEAHPGG hHHHh

		1.0					
MOUSEPRO.DNA	,	10					
HUMANPRO DNA	1	TCGGITIGGA	TATCATGGGA	TG-GAATGAG	AAGGGA-AAG	TAGGAGCCCG	50
HOURING NO. DIA	1	FAGGGTTGGA				TACAGTCATG	50
MOUSEPRO.DNA	5.1				90		
HUMANPRO DNA	51	CAACTCTAAA	AAGACAAG	ACATTTTGAG	TGTCTGACAA	ATTCTTCATA	100
	31	110	120				100
MOUSEPRO.DNA	101			130 ATTCAGTCTG	140		
HUMANPRO. DNA	101	TALAAATTAA	CCCCAMAMAC	AGAAAAGTCA	TATAGGTTAT	TTCTATAGGA	150
	101	160	170	180			150
MOUSEPRO.DNA	151			CTTGTGCACT	190	200	
HUMANPRO, DNA				AGAGTGTTTT			200
		210	220	230	240		200
MOUSEPRO.DNA	201			ATGTCCAGTT		250	050
HUMANPRO. DNA				A-GTCATTTT			250
		260	270	280	290		250
MOUSEPRO. DNA	251			GAAAGTGCGC		300	200
HUMANPRO.DNA				AGAAATCTTA			300
		310	320	330	340	350	300
MOUSEPRO. DNA	301			CAGTTA			350
HUMANPRO. DNA				TCTCTAACTG			350
		360	370	380	390	400	330
MOUSEPRO. DNA	351	AAAGTCTT		GTTAGAGA			400
HUMANPRO. DNA				GTTAGAAAAC			400
		410	420	430	440	450	100
MOUSE PRO. DNA	401	ATGGTGGTAC	ACACCTGTGA	TCTCTGTGTT			450
HUMANPRO.DNA				ACCAAGTGGC			450
		460	470	480	490	500	
MOUSEPRO. DNA	451	ATCAGGAGTT	CAAGGCCAGC	CTGAGCTACT	TGAGACCCAG	TCTAAATAAA	500
HUMANPRO.DNA				AAGCAA			500
		510	520	530	540	550	
MOUSEPRO.DNA				GCCTTTAACT			550
HUMAN PRO. DNA	501	CTACCTGCAG	AA-AGAAAGG	GCAAAGATGC	TGTAGGCAAG	AGAAGTTCAG	550
		560	570	580	590	600	
MOUSEPRO.DNA				CTGAAATAAT			600
HUMAN PRO. DNA	551		GGCATA-G	CTCAAA-GAT	T.CACATTTGA	GCAGC	600
		610	620	630	640	650	
MOUSEPRO.DNA				G-GTCAGTAT			650
HUMAN PRO. DNA	601			TTACCAAAAT	GT-CGAAGGG	CAAAGGAG	650
MOUSERDO DA		660	670	680	690	700	
MOUSEPRO.DNA	651	ACCCCCAGCT	CCTGAGCTGA	GTGATGGGGA	AGGACAGCCA	CTGCCTGTGA	700
HUMAN PRO. DNA	651			-TGATGA		TGTCCTTT	700
MOUSEPRO. DNA	701	710	720	730	740	750	
HUMAN PRO. DNA	701	TGTGTGAGTG	ACGTGCTTCC	AAGTGTTTTA	ACCACTGACG	ATTACATAGC	750
HOLENTE KO. DNA	/01			AGACATTTAT			750
MOUSEPRO.DNA	751	760	770	780	790	800	
HUMAN PRO. DNA	751	CABACAGTC	AGGAGAAAAC	AGCCGTATTC	TUTGCCAGTT	CTCTTCCCTT	800
	131			A-CTTTTTTC			800
MOUSE PRO. DNA	201	810	820	830 CACACAGAGA	840	850	
HUMAN PRO. DNA				CACACAGAGA . AGT-CAACTG			850
	301	860	870	AGI-CAACIG 880			850
		300	0,0	000	890	900	

FIGURE 8 cont'd

MOUSEPRO.DNA	851	TTTGTTCTGA	TTAGGGGCAA	TTTTAAGTAC	TTAAGAGTTC	ACACAAAGTC	900
HUMANPRO.DNA	851	TTTGTTACAC	TTAGAAACTT	CTAAAAGTGC	TTAAGATTTC	ACCTGAAAGT	900
		910	920	930	940	950	
MOUSEPRO.DNA	901	TAGCCTTCAA	AAAGAAAACA	GGTTCCCAAA	CTA	-GGGAGGAAA	950
HUMANPRO.DNA	901	CCAACAT-GA	AGAAAATACA	GGCTCCCCAA	TGCCCCATTC	TAAGAAGAAA	950
		960	970	980	990	1000	
MOUSEPRO.DNA	951	CAGAATCATT	TCCATTTTGG	TGACATTTA-	GTGGGAAGAA	GCTCACAGAC	1000
HUMANPRO.DNA	951	AAGGACCATT	TTCATTTTAG	TAACGTTTCT	GTTCTATAGA	CAGTTTGGAT	1000
		1010	1020	1030	1040	1050	
MOUSEPRO.DNA				TCCCCACTAG			1050
HUMANPRO.DNA	1001	AACTAGCTCT	TACTTTTAT	CTTTAAAAAC	TGTTTTTCCA	GTGAAGTTAC	1050
		1060	1070	1080	1090	1100	
MOUSEPRO.DNA				CACTGGTATT			1100
HUMANPRO.DNA	1051	GTATAATTAT	TTACTTCAAG	CG-TAGTATA	CCAAATTACT	TTAGAAATGC	1100
		1110	1120	1130	1140	1150	
MOUSEPRO.DNA	1101	AAGACTTTCC	TTGTGCTTTA	CTAAAAAC-C	CA-GACGGTG	AATCTTGAAT	1150
HUMANPRO.DNA	1101	AAGACTTTTC	TTATACTTCA	TAAAATACAT	TATGAAAGTG	AATCTTGT	1150
		1160	1170	1180	1190	1200	
MOUSEPRO.DNA				CAGGCATTCT			1200
HUMANPRO.DNA	1151	TGGCTGTGTA	CATTTGACTA	TAATAATTTC	AATGCATATT	ATTTCTATTG	1200
		1210	1220	1230	1240	1250	
MOUSEPRO.DNA				GCTGGCTGCG			1250
HUMANPRO.DNA	1201		ACAGTTTTTG	GCAAACTGCG	TTTGATGAGG	GCTATCTCCT	1250
		1260	1270	1280	1290	1300	
MOUSEPRO.DNA				CT-GTGATGC			1300
HUMANPRO.DNA	1251		GTTTCTAAAA	CTTGTGATGC	AAACGCTCCC	ACCCTTTCCT	1300
		1310	1320	1330	1340	1350	
MOUSEPRO.DNA				TCAGGCGGCG			1350
HUMANPRO.DNA	1301	GGGAACACAG	AAAGCCTGAC	TCAGGCCATG	GCCGCTATTA	AAGCAGCTCC	1350
		1360	1370	1380	1390	1400	
MOUSEPRO. DNA				GGGCT-GCCG			1400
HUMANPRO.DNA	1351	AGCCCTGCGC	ACTCCCTGCT	GGGTGAGCAG	CACTGTAAAG	ATG	1400

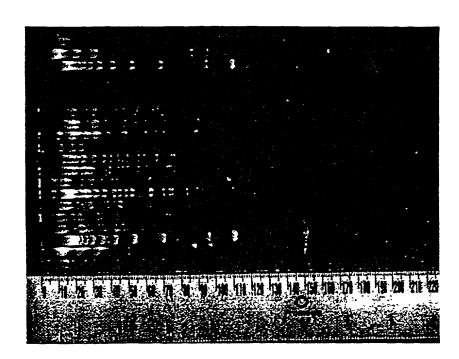
	<u>F</u> .	IGUKE	_9		
10	2	0	30	40	50
TAGGGTTGGAAG					
60	7		80	90	100
GAAGTGTAAAG	AGTCTGCC	AACATTTT	GAGAATGT		
110				140	150
AAAATTAAGGG					
		TCF1			
160	17	0	180	190	200
AAATATGAGAT					
GAT					OHIII I
210		0		240	250
GATTTTTGCCC					
		NF IL			
260	27	0	280	290	300
CCTTTTTAAAC	AAGAAATC'	TTATGAGA	TGTCAATA	TGCAAAACA	AATTAA
		_			
310			330		350
AAGGAGGTGGT	TTCTCTAA	ACTGAAGCT	rgttcctc:	TTTCCTGCCT	TCAGCC
TCF1					
360		70			400
TCTGAAGAGAA	AAGTTAGA?			TGCTACATG	TTTGAA
		NF_E1			
410			430		450
CAAGCTGATAT		GCCCAGAG	SAGCAGGT	AGAAGAACCA	AGCGTGG
	PHTH		400	400	500
460	-	70		.,,	500
AGACAGAAAGO	CAAGAGGCC		ALJJJJA		JUAAADE
510	ر ہے	2.0	5 20	NF IL6	550
510	52 CCT1 CCC1		530		550
GCAAAGATGCT TCF1	I G I AGGCAI	LOARDADA	I CAGGACA	GACAC I GGCI	ATAGCIL
560	53	70	580	590	600
:AAAGATTCACA	ATTTGAGC.	<u>AGCTG</u> TGG.	AAGATGAC.	AGTACAATT	ACCAAAA
TCF1	PHTH 1	bHLH			
]	E2A			
610		20	630	640	650
TGTCGAAGGG	CAAAGGAG	GCAGCTAC			AATTATG
	TCF1			NF ILE	
660	_	70	680	690	700
TCCTTTTAAA'					
710		20	730	740	750
GG <u>ACAAAG</u> GA. TCF1	ATAGAAAG	TAGCACTT	TTTTCTCC	ACTAGTTTT	CTTCTCT
760	7	70	780	790	800
TTTTCAAGTA					GCTGTAC
			HLH		
	SUBSTITU	TE SHEET	(RULE 26)		-

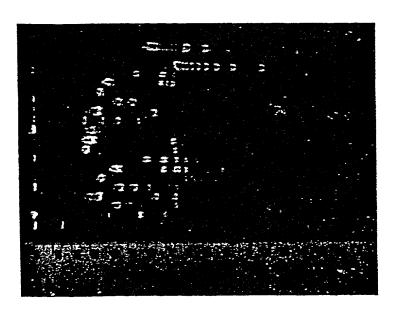
FIGURE 9 CONT'D

8	10	820	830	840	850
TTTGTTAC	ACTTAGAA	ACTTCTAA	AAGTGCTTAA	GATTTCACCT	GAAACG
		TCI	F1	bHL	
	60	870	880	890	900
CCAACATG	aagaaaat	FACAGGCTC	CCAATGCCC	CATTCTAAGA	AGAAAA
9	10	920	930	940	950
AGGACCAT	TTTCATTI	TAGTAACGT	TTTCTGTTCT	ATAGACAGTI	TGGATA
9	60	970	980	990	1000
ACTAGCTC	TTACTTT	TATCTTTAL	AAAACTGTTT	TTCCAGTGAA	GTTACG
10		1020			1050.
TATAATTA	TTTACTTC	CAAGCGTAGT	TATACCAAAT	TACTTTAGAA	ATGCAA
				NF II	.6
10		1070			1100
GACTTTTC	TTATACTI	CATAAAATA	CATTATGAA	<u>AG</u> TGAATCTT	GTTGGC
			NF IL6		
11		1120		1140	
TGTGTACA	<u>TTTG</u> ACTA	TAATAATT	CAATGCATA'	TTATTTCTAT	TGAGAG
	HLH				
11			1180		
TAAGTTAC	AGTTTTTG		CGTTTGATGA		CTCTTC
12			1230		1250
CIGIGCGT	TTCTAAAA		CAAACGCTC	CCACCCTTTC	CTGGGA
4.0		AABS			
12		1270			1300
	ACGCIGAC	TCAGGCACG	TGCCGCTAT		CCAGCC
+1		bhle 1000		box	
13	_	1320			
しょいいしんしんし	111111111	GGG I GAGCA	GCACTGTAA	A CATC	

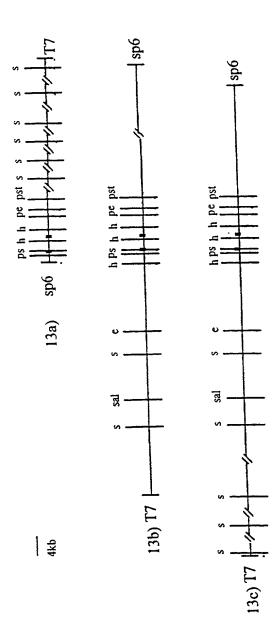
FIGURE 10A

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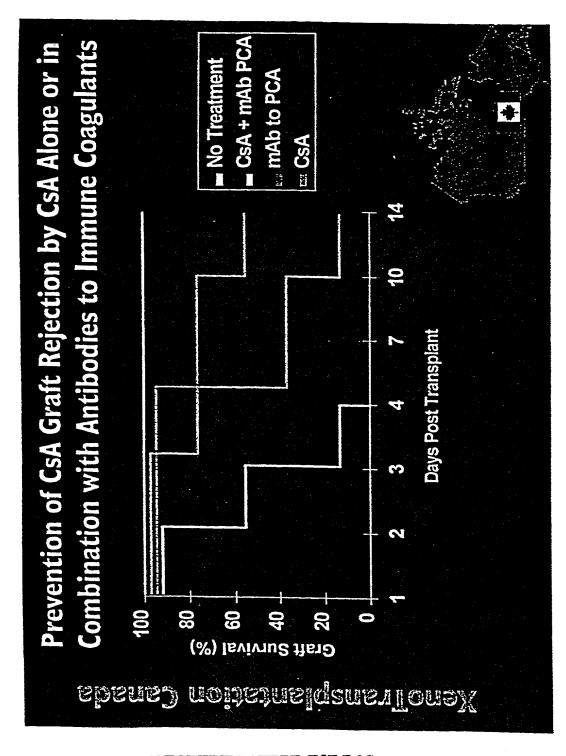




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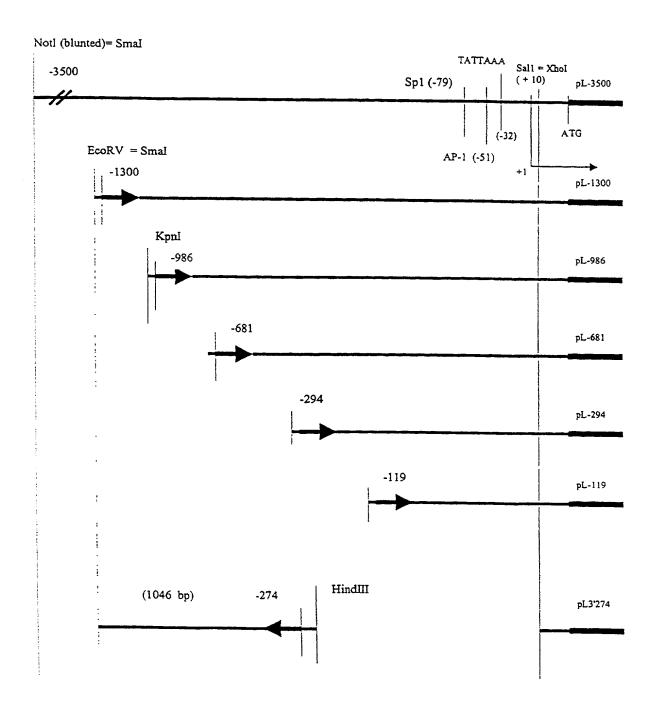


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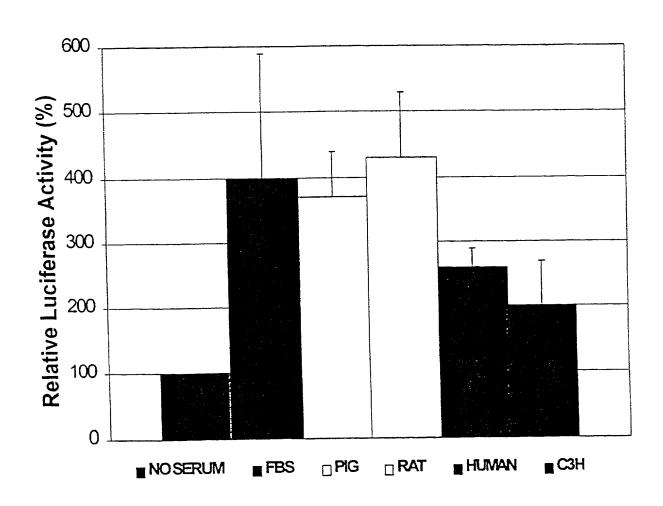


SUBSTITUTE SHEET (RULE 26)

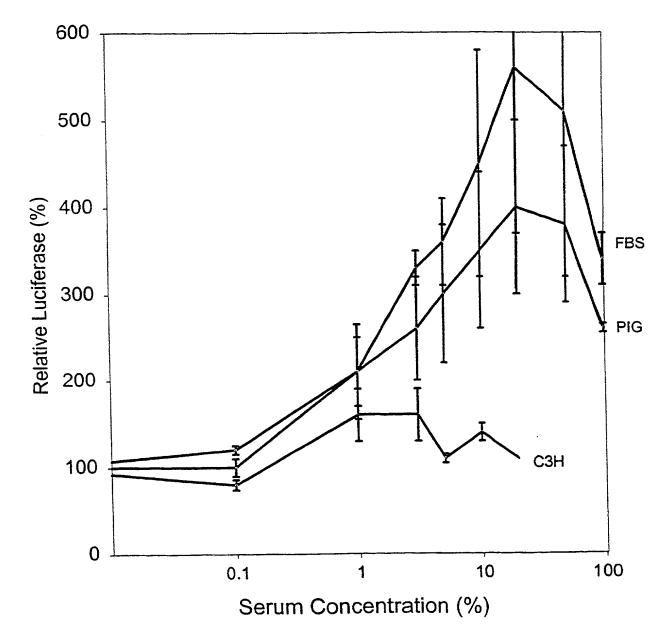
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17/24 FIGURE 15



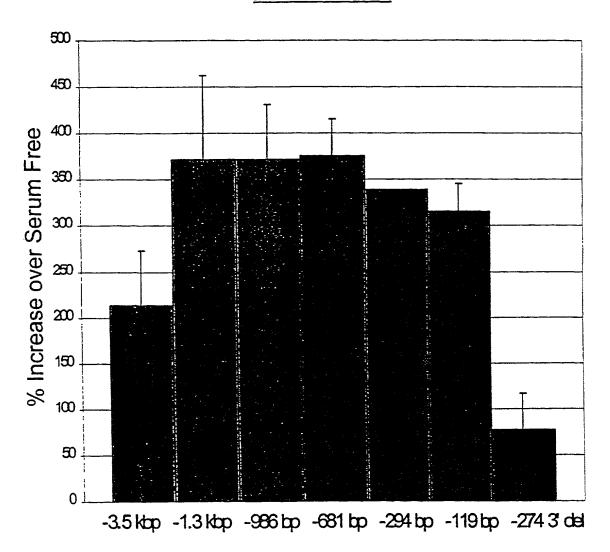
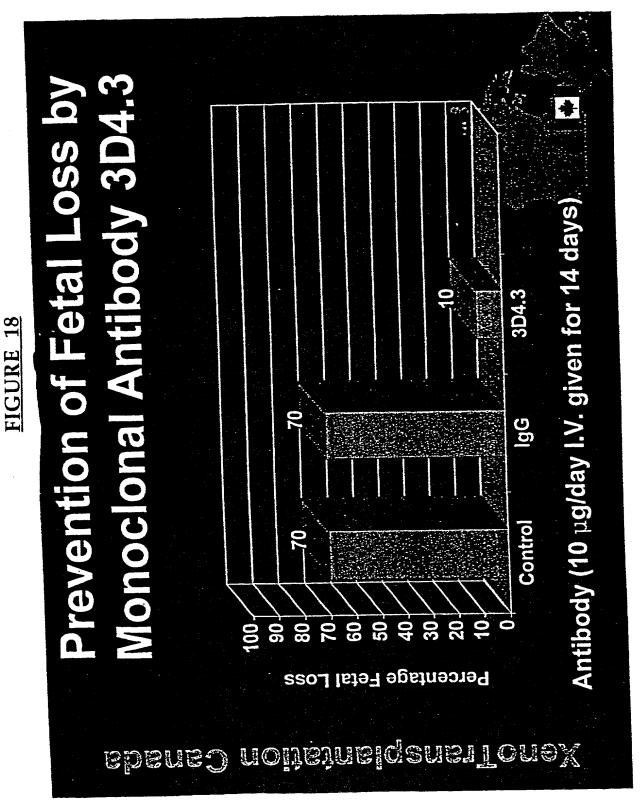


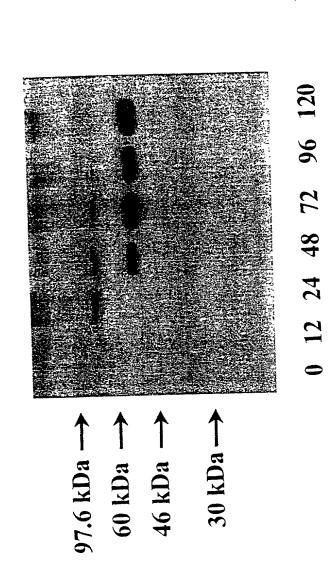
FIGURE 17

5'	CCAAGTATA	T AATATGG1	TAT CTITI	rgggca ·	CTGGTATTAC	AACTGTTTTT	-2/0
	TAAACAAAA	G ACTTTCCT	TG TGCT	TTACTA	AAAACCCAGA	CGGTGAATCT	-220
	TGAATACAA	T GCGTGGC	ACC CACC	GCAGGC	ATTCTATTGT	GCATAGTTTT	-170
	GACTGACAC	G AGATGAC	AGC ATTI	GGCTGC	GTGCGCTTGC	TGAGGACCCT	-120
	CTCCTCCTG	T GTGGCGTC	CTG AGA	CTGTGAT	GCAAATGCGC	CCGCCCTTTT	-70
	CTGGGAACI	C AGAANGO	CTG AGT	CAGGCG	G CGGTGGCTAT	TAAAGCGCC	T-20
	GGTCAGGCT	rg ggctgcc	GCA CTCC	CAAGG3	•		

+1



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TIGURE 19

The lanes are:

H5cells
 H5 + wild type virus

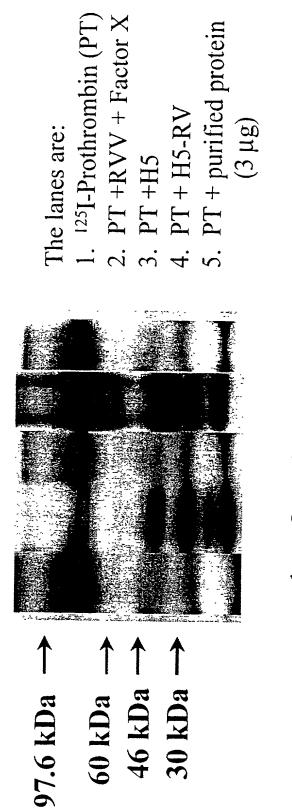
H5 + recombinant

97.6 kDa 60 kDa

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The lanes are:
1. H5cells
2. H5 + wild type virus
3. H5 + recombinant
virus 97.6 kDa →
60 kDa →
46 kDa →

IGURE 2



The lanes are: